

Tany



PCT10

RAW SEQUENCE LISTING

DATE: 06/12/2002

PATENT APPLICATION: US/10/049,358

TIME: 12:22:42

Input Set : A:\10-049,358-Sequence Listing.txt

Output Set: N:\CRF3\06122002\J049358.raw

3 <110> APPLICANT: Davis, Maria
 4 Nelson, John
 5 Kumar, Shiv
 6 Finn, Patrick
 7 Nampalli, Satyam
 8 Flick, Parke
 10 <120> TITLE OF INVENTION: TAQ DNA Polymerase Having an Amino Acid Substitution at
 11 E681 and Homologs Thereof Exhibiting Improved Salt
 12 Tolerance
 14 <130> FILE REFERENCE: PB9944
 16 <140> CURRENT APPLICATION NUMBER: 10/049,358
 C--> 17 <141> CURRENT FILING DATE: 2002-05-17
 19 <150> PRIOR APPLICATION NUMBER: PCT/US00/22150
 20 <151> PRIOR FILING DATE: 2000-08-10
 22 <150> PRIOR APPLICATION NUMBER: 60/148,012
 23 <151> PRIOR FILING DATE: 1999-08-10
 25 <160> NUMBER OF SEQ ID NOS: 3
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 832
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Thermus aquaticus
 34 <400> SEQUENCE: 1
 35 Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
 36 1 5 10 15
 38 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
 39 20 25 30
 41 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 42 35 40 45
 44 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
 45 50 55 60
 47 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
 48 65 70 75 80
 50 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
 51 85 90 95
 53 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
 54 100 105 110
 56 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
 57 115 120 125
 59 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
 60 130 135 140
 62 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
 63 145 150 155 160

ENTERED

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65 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
66          165          170          175
68 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
69          180          185          190
71 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
72          195          200          205
74 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
75          210          215          220
77 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
78 225          230          235          240
80 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
81          245          250          255
83 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
84          260          265          270
86 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
87          275          280          285
89 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
90          290          295          300
92 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
93 305          310          315          320
95 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
96          325          330          335
98 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
99          340          345          350
101 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
102          355          360          365
104 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
105          370          375          380
107 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
108 385          390          395          400
110 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
111          405          410          415
113 Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
114          420          425          430
116 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
117          435          440          445
119 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
120          450          455          460
122 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
123 465          470          475          480
125 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
126          485          490          495
128 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
129          500          505          510
131 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
132          515          520          525
134 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
135          530          535          540
137 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu

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138 545          550          555          560
140 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
141          565          570          575
143 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
144          580          585          590
146 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
147          595          600          605
149 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
150          610          615          620
152 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
153 625          630          635          640
155 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
156          645          650          655
158 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
159          660          665          670
161 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
162          675          680          685
164 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
165          690          695          700
167 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
168 705          710          715          720
170 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
171          725          730          735
173 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
174          740          745          750
176 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
177          755          760          765
179 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
180          770          775          780
182 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
183 785          790          795          800
185 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
186          805          810          815
188 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
189          820          825          830
195 <210> SEQ ID NO: 2
196 <211> LENGTH: 560
197 <212> TYPE: PRT
198 <213> ORGANISM: Thermus aquaticus
200 <400> SEQUENCE: 2
201 Met Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
202 1          5          10          15
204 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
205          20          25          30
207 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
208          35          40          45
210 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
211          50          55          60
213 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu

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```

214 65          70          75          80
216 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
217          85          90          95
219 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
220          100          105          110
222 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
223          115          120          125
225 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
226          130          135          140
228 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
229 145          150          155          160
231 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
232          165          170          175
234 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
235          180          185          190
237 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
238          195          200          205
240 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
241          210          215          220
243 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
244 225          230          235          240
246 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
247          245          250          255
249 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
250          260          265          270
252 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
253          275          280          285
255 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
256          290          295          300
258 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
259 305          310          315          320
261 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Gly Trp Leu Leu Val
262          325          330          335
264 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
265          340          345          350
267 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
268          355          360          365
270 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
271          370          375          380
273 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Tyr Gly Val Leu Tyr
274 385          390          395          400
276 Gly Met Ser Ala His Arg Leu Ser Gln Arg Leu Ala Ile Pro Tyr Glu
277          405          410          415
279 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
280          420          425          430
282 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
283          435          440          445
285 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
286          450          455          460

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```

288 Arg Val Lys Ser Val Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
289 465                               470                               475                               480
291 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
292                               485                               490                               495
294 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
295                               500                               505                               510
297 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
298                               515                               520                               525
300 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
301                               530                               535                               540
303 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
304 545                               550                               555                               560
310 <210> SEQ ID NO: 3
311 <211> LENGTH: 830
312 <212> TYPE: PRT
313 <213> ORGANISM: Thermus aquaticus
315 <400> SEQUENCE: 3
316 Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
317 1                               5                               10                               15
319 Val Ala Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
320                               20                               25                               30
322 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
323                               35                               40                               45
325 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
326                               50                               55                               60
328 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
329 65                               70                               75                               80
331 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
332                               85                               90                               95
334 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
335                               100                              105                              110
337 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
338                               115                              120                              125
340 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
341                               130                              135                              140
343 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
344 145                               150                              155                              160
346 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
347                               165                              170                              175
349 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
350                               180                              185                              190
352 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
353                               195                              200                              205
355 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
356                               210                              215                              220
358 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
359 225                               230                              235                              240
361 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
362                               245                              250                              255

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/049,358

DATE: 06/12/2002

TIME: 12:22:43

Input Set : A:\10-049,358-Sequence Listing.txt

Output Set: N:\CRF3\06122002\J049358.raw

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date